

B' concl
complementary to said target nucleic acid sequence except that the group of probes includes all possible monosubstitutions of positions in said sequence that are within n bases of a base in said sequence that is complementary to said polymorphism, wherein n is from 0 to 5, and a second and third group of probes complementary to marker-specific regions upstream and downstream of the polymorphism in the target nucleic acid sequence, wherein the third group of probes differs from the second set of probes at single bases corresponding to known mismatch positions.

2. The array of claim 1, wherein the polymorphism is identified as a result of Principal Component Analysis of hybridization intensities of the array of probes.
3. The array of claim 1, wherein at least two alleles of the polymorphism are known.
4. The array of claim 1, wherein said first groups of probes comprises a plurality of different probes that are complementary to overlapping portions of said target nucleic acid sequence.
5. The array of claim 1, wherein the monosubstitutions occur at a plurality of distances from a 3' end of said probes.
6. The array of claim 1, wherein said detection block includes between about 8 and 88 different probes.
7. The array of claim 1, comprising between 1 and 1,000 different detection blocks, each of said detection blocks including probes complementary to different polymorphisms in said target nucleic acid sequence.

8-17. (Canceled)

8 18. (New) An array of oligonucleotide probes for detecting a polymorphism in a target nucleic acid sequence, said array comprising:

a first group of probes that are complementary to said target nucleic acid sequence except that the group of probes includes all possible monosubstitutions of positions in said sequence that are within n bases of a base in said sequence that is complementary to said polymorphism; and
a second and third group of probes complementary to marker-specific regions upstream and downstream of the polymorphism in the target nucleic acid sequence, wherein the third

group of probes differs from the second set of probes at single bases corresponding to known mismatch positions.

~~9~~ ~~19~~. (New) The array of claim ~~18~~⁸, wherein at least two alleles of the polymorphism are known.

~~10~~ ~~20~~. (New) The array of claim ~~18~~⁸, wherein said first groups of probes comprises a plurality of different probes that are complementary to overlapping portions of said target nucleic acid sequence.

~~11~~ ~~21~~. (New) The array of claim ~~18~~⁸, wherein the monosubstitutions occur at a plurality of distances from a 3' end of said probes.

~~12~~ ~~22~~. (New) The array of claim ~~18~~⁸, wherein said detection block includes between about 8 and 88 different probes.

~~13~~ ~~23~~. (New) The array of claim ~~18~~⁸, comprising between 1 and 1,000 different detection blocks, each of said detection blocks including probes complementary to different polymorphisms in said target nucleic acid sequence.